

# Package ‘GSE62944’

September 3, 2024

**Title** GEO accession data GSE62944 as a SummarizedExperiment

**Description** TCGA processed RNA-Seq data for 9264 tumor and 741 normal samples across 24 cancer types and made them available as GEO accession [GSE62944](http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE62944). GSE62944 data have been parsed into a SummarizedExperiment object available in ExperimentHub.

**Version** 1.33.0

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**URL** <http://bioconductor.org/packages/release/bioc/html/GSE62944.html>

**biocViews** ExperimentData, Genome, DNASEqData, RNASeqData

**Depends** Biobase, GEOquery

**Suggests** ExperimentHub (>= 0.99.6), knitr, BiocStyle, rmarkdown, DESeq2

**License** Artistic-2.0

**VignetteBuilder** knitr

**NeedsCompilation** no

**git\_url** <https://git.bioconductor.org/packages/GSE62944>

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GSE62944-package

*GEO accession GSE62944 available as an ExpressionSet object.*

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## Description

TCGA re-processed RNA-Seq data from 9264 Tumor Samples and 741 normal samples across 24 cancer types and made it available as GEO accession [GSE62944](<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE62944>)  
These data have been parsed into a SummarizedExperiment objects and are available in ExperimentHub.

## Details

See the vignette for examples of using these data in differential gene expression analysis.

```
browseVignettes("GSE62944")
```

Details of how these data were created are in the scripts/ directory of the source package.

## Examples

```
library(ExperimentHub)
hub <- ExperimentHub()
x <- query(hub, c("GSE62944", "tumor"))
x
y <- query(hub, c("GSE62944", "normal"))
y
## Not run:
## download resource
se_tumor = x[[1]]
se_normal = y[[1]]

## End(Not run)
```

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\* **utilities**

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